

SEQ SEARCH SUMMARY

10/070480

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 20:41:39 ; Search time 163 Seconds
(without alignments)
718.947 Million cell updates/sec

Title: US-10-070-480A-2
Perfect score: 1614
Sequence: 1 TRQMILAVGQQGPIARAETR.....HIFNFKQHRQPQHYGLIAEL 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1614	100.0	303	2	AAR46267	Aar46267 Improved
2	1614	100.0	303	4	AAB74625	Aab74625 Escherich
3	1614	100.0	303	6	ABP59067	Abp59067 Decarbamy
4	1611	99.8	303	2	AAR46266	Aar46266 Improved
5	1610	99.8	303	2	AAR46262	Aar46262 Improved
6	1609	99.7	303	2	AAR46261	Aar46261 Improved
7	1609	99.7	303	2	AAR46272	Aar46272 Improved
8	1609	99.7	303	2	AAR46265	Aar46265 Improved
9	1608	99.6	303	2	AAR46257	Aar46257 Improved

NO 1994
NO 2001 Appl
JP 2002

xtul
xtul

10	1606	99.5	303	2	AAR46260	Aar46260	Improved
11	1606	99.5	303	2	AAR46264	Aar46264	Improved
12	1606	99.5	303	2	AAR46271	Aar46271	Improved
13	1605	99.4	303	2	AAR46245	Aar46245	Heat-stab
14	1605	99.4	303	2	AAR46263	Aar46263	Improved
15	1605	99.4	303	2	AAR46269	Aar46269	Improved
16	1605	99.4	303	2	AAR46256	Aar46256	Improved
17	1605	99.4	303	2	AAR46270	Aar46270	Improved
18	1604	99.4	303	2	AAR46259	Aar46259	Improved
19	1604	99.4	303	2	AAR46240	Aar46240	Heat-stab
20	1603	99.3	303	2	AAR46244	Aar46244	Heat-stab
21	1603	99.3	303	2	AAR46268	Aar46268	Improved
22	1603	99.3	303	2	AAR46249	Aar46249	Heat-stab
23	1603	99.3	303	2	AAR46243	Aar46243	Heat-stab
24	1601	99.2	303	2	AAR46258	Aar46258	Improved
25	1600	99.1	303	2	AAR46242	Aar46242	Heat-stab
26	1600	99.1	303	2	AAR46252	Aar46252	Heat-stab
27	1600	99.1	303	2	AAR46246	Aar46246	Heat-stab
28	1600	99.1	303	2	AAR46250	Aar46250	Heat-stab
29	1600	99.1	303	2	AAR46253	Aar46253	Heat-stab
30	1599	99.1	303	2	AAR46239	Aar46239	Heat-stab
31	1599	99.1	303	2	AAR46255	Aar46255	Improved
32	1599	99.1	303	2	AAR46251	Aar46251	Heat-stab
33	1599	99.1	303	4	AAB74624	Aab74624	Agrobacte
34	1599	99.1	303	6	ABP59068	Abp59068	Decarbamy
35	1597	98.9	303	2	AAR46241	Aar46241	Heat-stab
36	1596	98.9	303	2	AAR46248	Aar46248	Heat-stab
37	1596	98.9	303	2	AAR46247	Aar46247	Heat-stab
38	1594	98.8	303	6	ABP59066	Abp59066	Decarbamy
39	1590	98.5	304	7	ADL07572	Adl07572	R. picket
40	1586	98.3	303	2	AAR25358	Aar25358	KNK-712.
41	1586	98.3	303	2	AAR46254	Aar46254	Heat-stab
42	1558	96.5	304	8	ADP43018	Adp43018	Agrobacte
43	1554	96.3	304	2	AAR53639	Aar53639	Carbamoyl
44	1554	96.3	304	2	AAR82836	Aar82836	Agrobacte
45	1548	95.9	304	8	ADP43019	Adp43019	Agrobacte

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OM protein - protein search, using sw model

Run on: June 7, 2005, 20:57:41 ; Search time 156 Seconds
(without alignments)
744.553 Million cell updates/sec

Title: US-10-070-480A-2
Perfect score: 1614
Sequence: 1 TRQMILAVGQQGPIARAETR.....HIFNFKQHRQPQHYGLIAEL 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1533	95.0	304	14	US-10-105-251-1	FD 2002	Sequence 1, Appli
2	1351	83.7	307	14	US-10-190-471-4		Sequence 4, Appli
3	1327	82.2	304	14	US-10-189-389-4		Sequence 4, Appli
4	1327	82.2	304	17	US-10-961-116-4		Sequence 4, Appli
5	789	48.9	315	14	US-10-105-294B-2		Sequence 2, Appli
6	789	48.9	315	14	US-10-105-251-2		Sequence 2, Appli
7	347.5	21.5	267	15	US-10-072-012-803		Sequence 803, App
8	315	19.5	280	14	US-10-156-761-9488		Sequence 9488, Ap
9	313	19.4	280	14	US-10-156-761-9491		Sequence 9491, Ap
10	306	19.0	299	15	US-10-424-599-176307		Sequence 176307,
11	299	18.5	299	15	US-10-424-599-176309		Sequence 176309,
12	287.5	17.8	308	16	US-10-425-115-271413		Sequence 271413,
13	287.5	17.8	309	15	US-10-425-114-45522		Sequence 45522, A
14	281	17.4	298	16	US-10-767-701-38053		Sequence 38053, A
15	280.5	17.4	301	16	US-10-437-963-188445		Sequence 188445,
16	263.5	16.3	301	16	US-10-739-930-8040		Sequence 8040, Ap
17	251.5	15.6	291	16	US-10-474-776-658		Sequence 658, App
18	251.5	15.6	291	17	US-10-472-928-1800		Sequence 1800, Ap
19	244	15.1	292	15	US-10-335-977-6533		Sequence 6533, Ap
20	239	14.8	276	9	US-09-855-294B-1		Sequence 1, Appli
21	239	14.8	276	10	US-09-769-952-2		Sequence 2, Appli
22	239	14.8	276	17	US-10-920-089-2		Sequence 2, Appli
23	239	14.8	285	10	US-09-769-952-14		Sequence 14, Appl
24	239	14.8	285	17	US-10-920-089-14		Sequence 14, Appl
25	232	14.4	276	9	US-09-855-294B-2		Sequence 2, Appli
26	217.5	13.5	188	16	US-10-425-115-271411		Sequence 271411,
27	213.5	13.2	313	14	US-10-146-772-150		Sequence 150, App
28	213.5	13.2	313	15	US-10-241-742-150		Sequence 150, App
29	213.5	13.2	313	15	US-10-440-523-150		Sequence 150, App
30	213.5	13.2	313	15	US-10-440-503-150		Sequence 150, App
31	213.5	13.2	313	15	US-10-461-925-150		Sequence 150, App
32	213	13.2	266	9	US-09-738-626-6568		Sequence 6568, Ap
33	213	13.2	266	17	US-10-494-675-116		Sequence 116, App
34	212	13.1	442	16	US-10-739-930-9954		Sequence 9954, Ap
35	209	12.9	384	15	US-10-220-381-5		Sequence 5, Appli
36	208	12.9	332	14	US-10-146-772-244		Sequence 244, App
37	208	12.9	332	15	US-10-241-742-244		Sequence 244, App
38	208	12.9	332	15	US-10-440-523-244		Sequence 244, App
39	208	12.9	332	15	US-10-440-503-244		Sequence 244, App
40	208	12.9	332	15	US-10-461-925-244		Sequence 244, App
41	207	12.8	367	15	US-10-425-114-63628		Sequence 63628, A
42	204.5	12.7	337	16	US-10-437-963-174139		Sequence 174139,
43	202	12.5	314	14	US-10-146-772-104		Sequence 104, App
44	202	12.5	314	15	US-10-241-742-104		Sequence 104, App
45	202	12.5	314	15	US-10-440-523-104		Sequence 104, App

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OM protein - protein search, using sw model

Run on: June 7, 2005, 20:42:04 ; Search time 40 Seconds
(without alignments)
728.842 Million cell updates/sec

Title: US-10-070-480A-2
Perfect score: 1614
Sequence: 1 TRQMILAVGQQGPIARAETR.....HIFNFKQHRQPQHYGLIAEL 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1599	99.1	304	2	JW0082	N-carbamyl-D-amino
2	941	58.3	312	2	JW0083	N-carbamyl-D-amino
3	305	18.9	280	2	T34905	probable hydrolase
4	304	18.8	262	2	C71109	hypothetical prote
5	303	18.8	280	2	T28684	hypothetical prote
6	289	17.9	262	2	C75051	hydrolase related
7	285	17.7	295	2	H82556	beta-alanine synth
8	280	17.3	297	2	F75263	probable hydrolase
9	269	16.7	272	2	T41662	probable nitrilase
10	261.5	16.2	272	2	B69109	N-carbamoyl-D-amin
11	252.5	15.6	292	2	G83608	probable hydratase
12	252	15.6	290	2	B81369	probable hydrolase
13	251.5	15.6	291	2	E95106	carbon-nitrogen hy

300/304

Nanba 1998

Agro. sp.
Pseudosp.

14	248	15.4	292	2	E64614	beta-alanine synth
15	246.5	15.3	291	2	G97974	beta-ureidopropion
16	244	15.1	292	2	F71901	hypothetical prote
17	243	15.1	220	2	A84673	probable nitrilase
18	241	14.9	294	2	AB0115	probable carbon-ni
19	240	14.9	292	2	C87275	hydrolase, carbon-
20	233.5	14.5	579	2	AH3225	amidohydrolase [im
21	220	13.6	285	2	S58240	hypothetical prote
22	213	13.2	283	2	A87352	carbon-nitrogen hy
23	213	13.2	298	2	T17568	hydrolase homolog
24	211	13.1	264	2	T36488	probable hydrolase
25	209.5	13.0	294	2	G71949	hypothetical prote
26	207.5	12.9	345	2	JC1174	amidase (EC 3.5.1.
27	206	12.8	387	2	T16068	hypothetical prote
28	205	12.7	284	2	AD3275	beta-ureidopropion
29	205	12.7	296	2	AI1530	conserved hypothet
30	204.5	12.7	346	2	A26741	amidase (EC 3.5.1.
31	201	12.5	257	2	C69264	conserved hypothet
32	201	12.5	346	2	H83222	aliphatic amidase
33	200	12.4	286	2	AE2988	amidohydrolase [im
34	200	12.4	290	2	C98295	hypothetical prote
35	199.5	12.4	259	2	E69863	conserved hypothet
36	199.5	12.4	270	2	B83387	hypothetical prote
37	198.5	12.3	260	2	D97105	probable amidohydr
38	198	12.3	271	2	G83780	hypothetical prote
39	196	12.1	576	2	G72277	NH(3)-dependent NA
40	195.5	12.1	292	2	E64558	conserved hypothet
41	194	12.0	334	2	F64674	aliphatic amidase
42	194	12.0	334	2	C71842	aliphatic amidase
43	193	12.0	296	2	AH1173	conserved hypothet
44	192	11.9	339	2	B71951	aliphatic amidase
45	190	11.8	339	2	F64556	aliphatic amidase

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OM protein - protein search, using sw model

Run on: June 7, 2005, 20:50:20 ; Search time 174 Seconds .
(without alignments)
891.724 Million cell updates/sec

Title: US-10-070-480A-2
Perfect score: 1614
Sequence: 1 TRQMILAVGQQGPIARAETR.....HIFNFKQHRQPQHYGLIAEL 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1599	99.1	304	1 DCAS_AGRSK	P60327 agrobacteri sp. Struclure
2	1590	98.5	304	2 Q8VTT6	Q8vtt6 burkholderi p. clustii
3	1554	96.3	304	1 DCAS_AGRU	Q44185 agrobacteri tumefaciens
4	1533	95.0	304	2 Q8VT65	Q8vt65 agrobacteri
5	959.5	59.4	319	2 Q89S29	Q89s29 bradyrhizob
6	941	58.3	312	2 Q76N51	Q76n51 pseudomonas
7	941	58.3	312	2 Q7M1B0	Q7mlb0 pseudomonas
8	820	50.8	310	2 Q89Q00	Q89q00 bradyrhizob
9	789	48.9	315	2 Q84FR7	Q84fr7 arthrobacte
10	774	48.0	307	2 Q89E80	Q89e80 bradyrhizob
11	352.5	21.8	296	2 Q846U4	Q846u4 brevibacill
12	330	20.4	291	2 Q8KCB4	Q8kcb4 chlorobium
13	315	19.5	280	2 Q82LR0	Q82lr0 streptomyce
14	313	19.4	280	2 Q82LQ7	Q82lq7 streptomyce
15	311	19.3	300	2 Q9XGI9	Q9xgi9 lycopersico

June 20
2000 Appl

16	309.5	19.2	284	2	Q7NJZ9	Q7njz9	gloeobacter
17	305	18.9	280	2	O69939	O69939	streptomyce
18	304	18.8	262	2	O58376	O58376	pyrococcus
19	303	18.8	280	2	O69808	O69808	streptomyce
20	292	18.1	290	2	Q7M8G2	Q7m8g2	wolinella s
21	289.5	17.9	299	2	Q9ZQH4	Q9zqh4	arabidopsis
22	289	17.9	262	2	Q9UYV8	Q9uyv8	pyrococcus
23	287.5	17.8	262	2	Q8U233	Q8u233	pyrococcus
24	287.5	17.8	326	2	Q8VYF5	Q8vyf5	arabidopsis
25	285	17.7	295	2	Q9PAQ2	Q9paq2	xylella fas
26	282.5	17.5	294	2	Q64TP9	Q64tp9	bacteroides
27	280.5	17.4	301	2	Q93XI4	Q93xi4	oryza sativ
28	280	17.3	297	2	Q9RRF7	Q9rrf7	deinococcus
29	279.5	17.3	294	2	Q8PK73	Q8pk73	xanthomonas
30	279.5	17.3	557	2	Q6N4F1	Q6n4f1	rhodopseudo
31	279	17.3	288	2	Q7URF9	Q7urf9	rhodopirell
32	279	17.3	292	2	Q87UB1	Q87ub1	pseudomonas
33	278	17.2	295	2	Q87BJ2	Q87bj2	xylella fas
34	269	16.7	272	2	O59829	O59829	schizosacch
35	269	16.7	281	2	Q972L1	Q972l1	sulfolobus
36	267.5	16.6	296	2	Q7VJA5	Q7vja5	helicobacte
37	267	16.5	294	2	Q8A9E0	Q8a9e0	bacteroides
38	266.5	16.5	264	2	Q972X1	Q972x1	sulfolobus
39	265.5	16.4	292	2	Q7MXM9	Q7mxm9	porphyromon
40	264	16.4	294	2	Q74ED5	Q74ed5	geobacter s
41	262.5	16.3	294	2	Q8P8P1	Q8p8p1	xanthomonas
42	261.5	16.2	272	2	O27839	O27839	methanobact
43	261.5	16.2	282	2	Q9Z5U5	Q9z5u5	zymomonas m
44	254.5	15.8	285	2	Q8DMK4	Q8dmk4	synechococc
45	253	15.7	579	2	Q6N746	Q6n746	rhodopseudo